AMENDMENT

In the Claims

The following Listing of Claims, in which deleted text appears **~~bolded struck through~~** or bolded in double brackets (*e.g.*, **[[deleted text]]**) and inserted text appears **bolded and underlined**, will replace all prior versions, and listings, of claims in the application.

Listing of Claims

1 – 42. (Canceled)

43. (Previously presented) A method for forming a catalogued nucleic acid library from an initial organism sample comprised of heterogeneous organisms, said method comprising:

(a) forming a derived organism sample from the initial heterogeneous organism sample by subjecting all or a part of said initial heterogeneous organism sample to a method of selection, such that proportional representations of the constituents in said derived organism sample are adjusted by subjecting all or a part of said initial heterogeneous organism sample to a method of positive and/or negative selection for at least one organism marker which is a nucleic acid marker characteristic of an organism in the initial organism sample;

(b) isolating an initial nucleic acid sample from said derived organism sample of step (a);

(c) forming a derived nucleic acid library from said isolated initial nucleic acid sample of step (b), such that the proportional representations of the constituents in said derived nucleic acid library are adjusted to advantage by performing the following steps in any order, and at least one time:

(i) subjecting all or a part of said initial nucleic acid sample to a period of selection,

(ii) recovering a fraction of said initial nucleic acid sample having at least one desired characteristic, and

(iii) assembling all or a part of said derived nucleic acid sample into a nucleic acid library;

thereby forming a catalogued nucleic acid library from the initial organism sample comprised of heterogeneous organisms.

44. (Previously presented) The method of claim 43 wherein the subjecting all or a part of said initial heterogeneous organism sample to a method of selection of step (a) further comprises: (i) resolving heterogeneity of the initial heterogeneous organism sample according to at least one organism marker such that the initial organism sample is normalized with respect to organisms exhibiting the at least one common organism marker before the subjecting all or a part of said initial organism sample to a method of selection; or (ii) resolving heterogeneity of the organism sample after the selection step of (a) but before step (b) by normalizing the initial organism sample with respect to organisms exhibiting the at least one common organism marker.

45. (Previously presented) The method of claim 44 wherein the at least one organism marker comprises a 16S rRNA content.

46. (Previously presented) The method of claim 43 wherein the subjecting all or a part of said initial heterogeneous organism sample to a method of selection of step (a) comprises selecting said initial heterogeneous organism sample using at least one organism marker such that the derived organism sample is selectively enriched with respect to organisms exhibiting the selected at least one organism marker.

47. (Previously presented) The method of claim 46 wherein the selected organisms in the derived organism sample exhibit increased 16S rRNA content or 18S rRNA content compared to those in the unselected initial organism sample.

48. (Previously presented) The method of claim 44 wherein step (a) further comprises initially resolving heterogeneity of said initial heterogeneous organism sample according to at least two organism markers.

49. (Previously presented) The method of claim 43 wherein step (c) comprises resolving heterogeneity of said initial nucleic acid sample according to at least one nucleic acid marker such that the derived nucleic acid library is normalized with respect to the nucleic acids exhibiting the at least one organism marker.

50. (Previously presented) The method of claim 49 wherein the at least one nucleic acid marker is G+C content of the nucleic acids in the derived nucleic acid library.

51. (Previously presented) The method of claim 43 wherein step (c) further comprises resolving heterogeneity of the initial nucleic acid sample according to at least one nucleic acid marker such that the derived nucleic acid library is selectively enriched with respect to nucleic acids exhibiting the at least one nucleic acid marker.

52. (Previously presented) The method of claim 51 wherein the at least one nucleic acid marker is G+C content of the nucleic acids in the derived nucleic acid library.

53. (Previously presented) The method of claim 43 wherein step (c) further comprises resolving heterogeneity of said initial nucleic acid sample according to at least two nucleic acid markers such that the derived nucleic acid library is advantageously adjusted with respect to nucleic acids exhibiting each of said nucleic acid markers.

54. (Previously presented) The method of claim 43 wherein step (c) comprises resolving heterogeneity of the initial nucleic acid sample according to at least one nucleic acid marker such that the derived nucleic acid library is normalized with respect to nucleic acids exhibiting the at least one nucleic acid marker.

55. (Previously presented) The method of claim 43 wherein the at least one organism marker comprises 18S rRNA.

56. (Previously presented) The method of claim 43 wherein the at least one organism marker comprises G+C content of the nucleic acids in the derived nucleic acid library.

57. (Previously presented) The method of claim 43 wherein step (c) comprises resolving heterogeneity of the initial nucleic acid sample according to at least one nucleic acid marker such that the derived nucleic acid library is selectively enriched with respect to nucleic acids that exhibit the at least one nucleic acid marker.

58. (Withdrawn - currently amended) The method of claim **[[81]]** 43 wherein the at least one organism marker comprises 16S rRNA content or 18S rRNA content.

59. (Withdrawn - currently amended) The method of claim **[[81]]** 43 wherein the at least one nucleic acid marker comprises G+C content of the nucleic acids in the derived nucleic acid library.

60. (Previously presented) The method of claim 80 wherein step (c) comprises resolving heterogeneity of said initial nucleic acid sample according to at least two nucleic acid markers such that the derived nucleic acid library is advantageously adjusted with respect to nucleic acids exhibiting each of said at least two nucleic acid markers.

61. (Canceled)

62. (Previously presented) The method of claim 80 wherein step (c) comprises resolving heterogeneity of said initial nucleic acid sample according to at least one nucleic acid marker such that the derived nucleic acid library is normalized with respect to nucleic acids that exhibit the at least one nucleic acid marker.

63. (Canceled)

64. (Canceled)

65. (Previously presented) The method of claim 80 wherein step (c) comprises resolving heterogeneity of said initial nucleic acid sample according to at least one nucleic acid marker such that the derived nucleic acid library is selectively enriched with respect to nucleic acids that exhibit the at least one nucleic acid marker.

66. (Previously presented) The method of claim 65 wherein the at least one organism marker comprises 16S rRNA content or 18S rRNA content.

67. (Previously presented) The method of claim 65 wherein the at least one nucleic acid marker comprises G+C content of nucleic acids.

68. (Previously presented) The method of claim 82 wherein step (c) comprises resolving heterogeneity of said initial nucleic acid sample according to at least two nucleic acid markers such that the derived nucleic acid library is advantageously adjusted with respect to nucleic acids that exhibit each of said at least two nucleic acid markers.

69. (Previously presented) The method of claim 68 wherein the at least one organism marker comprises 16S rRNA content or 18S rRNA content.

70. (Previously presented) The method of claim 82 wherein step (c) comprises resolving heterogeneity of said initial nucleic acid sample according to at least one nucleic acid marker such that the derived nucleic acid library is normalized with respect to nucleic acids that exhibit that at least one nucleic acid marker.

71. (Previously presented) The method of claim 70 wherein the at least one nucleic acid marker comprises the G+C content of nucleic acids.

72. (Previously presented) The method of claim 82 wherein step (c) comprises resolving heterogeneity of said initial nucleic acid sample according to at least one nucleic acid marker such that the derived nucleic acid library is selectively enriched with respect to nucleic acids that exhibit the at least one nucleic acid marker.

73. (Previously presented) The method of claim 72 wherein the at least one nucleic acid marker comprises G+C content of the nucleic acids in the derived nucleic acid library.

74. (Previously presented) The method of claim 80 wherein step (c) further comprises forming a genomic DNA library, thereby forming a catalogued genomic DNA library.

75. (Previously presented) The method of claim 43 wherein step (c) further comprises forming a genomic gene cluster DNA library, thereby forming a catalogued genomic gene cluster DNA library.

76. (Previously presented) The method of claim 43, wherein step (c) comprises forming a cDNA library, thereby forming a catalogued cDNA library.

77. (Previously presented) The method of claim 43 wherein step (a) further comprises forming a derived organism sample that consists essentially of environmental organisms.

78. (Previously presented) The method of claim 80 wherein step (a) comprises forming a derived organism sample that consists essentially of environmental organisms.

79. (Previously presented) The method of claim 82 wherein step (a) further comprises forming a derived organism sample that consists essentially of environmental organisms.

80. (Previously presented) A method for forming a catalogued nucleic acid library from an initial organism sample comprised of heterogeneous organisms, said method comprising:

(a) forming a derived organism sample from the initial heterogeneous organism sample, such that proportional representations of the constituents in said derived organism sample are adjusted to advantage by recovering a fraction of said initial heterogeneous organism sample having at least one organism marker which is a nucleic acid marker characteristic of an organism in the initial organism sample;

(b) isolating an initial nucleic acid sample from said derived organism sample; and

(c) forming a derived nucleic acid library from said isolated initial nucleic acid sample of step (b), such that the proportional representations of the constituents in said derived nucleic acid library are adjusted to advantage by performing the following steps in any order, and at least one time:

(i) subjecting all or a part of said initial nucleic acid sample to a period of selection,

(ii) recovering a fraction of said initial nucleic acid sample having at least one desired characteristic, and

(iii) assembling all or a part of said derived nucleic acid sample into a nucleic acid library;

thereby forming a catalogued nucleic acid library from the initial heterogeneous organism sample comprised of heterogeneous organisms.

81. (Canceled)

82. (Previously presented) A method for forming a catalogued nucleic acid library from an initial organism sample comprised of heterogeneous organisms, said method comprising:

(a) forming a derived organism sample from the initial heterogeneous organism sample, such that proportional representations of the constituents in said derived organism sample are adjusted to advantage by performing in any order both (i) subjecting all or a part of said initial heterogeneous organism sample to a method of positive and/or negative selection for at least one organism marker which is a nucleic acid marker characteristic of an organism in the initial organism sample, and (ii) recovering a fraction of said initial heterogeneous organism sample having at least one desired characteristic;

(b) isolating an initial nucleic acid sample from said derived organism sample; and

(c) forming a derived nucleic acid library from said isolated initial nucleic acid sample of step (b), such that the proportional representations of the constituents in said derived nucleic acid library are adjusted to advantage by performing the following steps in any order, and at least one time:

(i) subjecting all or a part of said initial nucleic acid sample to a period of selection,

(ii) recovering a fraction of said initial nucleic acid sample having at least one desired characteristic, and

(iii) assembling all or a part of said derived nucleic acid sample into a nucleic acid library;

thereby forming a catalogued nucleic acid library from the initial heterogeneous organism sample comprised of heterogeneous organisms.

83. (Previously presented) The method of claim 43 wherein the initial organism sample is a direct environmental sample.

84. (Previously presented) The method of claim 80 wherein the initial organism sample is a direct environmental sample.

85. (Previously presented) The method of claim 82 wherein the initial organism sample is a direct environmental sample.

86. (Previously presented) The method of claim 43 wherein the nucleic acid marker is a nucleic acid sequence.

87. (Previously presented) The method of claim 80 wherein the nucleic acid marker is a nucleic acid sequence.

88. (Previously presented) The method of claim 82 wherein the nucleic acid marker is a nucleic acid sequence.

89. (Previously presented) The method of claim 43 wherein the nucleic acid marker is an expressed protein product of a nucleic acid.

90. (Previously presented) The method of claim 80 wherein the nucleic acid marker is an expressed protein product of a nucleic acid.

91. (Previously presented) The method of claim 82 wherein the nucleic acid marker is an expressed protein product of a nucleic acid.

92. (Previously presented) The method of claim 43 wherein the nucleic acid marker is a biochemical process related to an expressed protein product of a nucleic acid.

93. (Previously presented) The method of claim 80 wherein the nucleic acid marker is a biochemical process related to an expressed protein product of a nucleic acid.

94. (Previously presented) The method of claim 82 wherein the nucleic acid marker is a biochemical process related to an expressed protein product of a nucleic acid.